FIG. 1A

```
atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac acc atc tcc cag   48
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
  1               5                  10                  15

gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta ggc   96
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
             20                  25                  30

aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag   144
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
         35                  40                  45

ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt   192
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
     50                  55                  60

atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac   240
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65                  70                  75                  80

tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc   288
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
                 85                  90                  95

atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg gac   336
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
            100                 105                 110

agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc   384
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
        115                 120                 125

acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc   432
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
    130                 135                 140

ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag   480
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145                 150                 155                 160

acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc tgg   528
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
                165                 170                 175

cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc   576
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
            180                 185                 190

tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag cag   624
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
        195                 200                 205
```

FIG. 1B

```
ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg gtg     672
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
    210                 215                 220

gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct aga     720
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225                 230                 235                 240

ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct gtc     768
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
                245                 250                 255

cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc atg     816
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
            260                 265                 270

ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa ttc     864
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
        275                 280                 285

tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga cac     912
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
    290                 295                 300

tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt cgc     960
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305                 310                 315                 320

agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg     1008
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
                325                 330                 335

caa tgg gat ccc cac att gtt gag tgg cac                             1038
Gln Trp Asp Pro His Ile Val Glu Trp His
            340                 345
```

FIG. 2A

```
gaaaaagaca aaaccagaaa aagaaaagtc atctccaggg ctcgatctag caacgagtct 60

gtagcatgta tagcgtcgga cccccgagct gcaacccaga aatgtacact cgtgggaaac 120

cgcttgcacc ccagagcctg acccagctgc aggcttcaac tctgtagggg acgtgcagct 180

cgtgatccaa gcctaggaga aaggacttgc tgccggcttt catttcctgg ctgaagtttc 240

tctcgtgggt gcagcgcctg catcccaggg tgatgaggtt aggggcccag ctgctagagg 300

agccctagtg ttcggatagg cagctgtgcc tctgtgccgg ccaccttgg atg cca gtc 358
                                                    Met Pro Val
                                                      1

ctc tct cca act gct atg gac aac ggg tcg tgc tgt ctc atc gag ggg   406
Leu Ser Pro Thr Ala Met Asp Asn Gly Ser Cys Cys Leu Ile Glu Gly
      5                  10                  15

gag ccc atc tcc cag gtg atg cct cct cta ctc atc ctg gtc ttc gtg   454
Glu Pro Ile Ser Gln Val Met Pro Pro Leu Leu Ile Leu Val Phe Val
 20                  25                  30                  35

ctt ggc gcc ctg ggc aac ggc ata gcc ctg tgc ggc ttc tgc ttt cac   502
Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe Cys Phe His
                 40                  45                  50

atg aag acc tgg aag tca agc act att tac ctt ttc aac ttg gct gtg   550
Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn Leu Ala Val
             55                  60                  65

gcc gat ttt ctc ctc atg atc tgc tta ccc ctt cgg aca gac tac tac   598
Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr Asp Tyr Tyr
         70                  75                  80

ctc aga cgc aga cac tgg att ttt gga gat atc gcc tgt cgc ctg gtc   646
Leu Arg Arg Arg His Trp Ile Phe Gly Asp Ile Ala Cys Arg Leu Val
     85                  90                  95

ctc ttc aag ctg gcc atg aat agg gcc ggg agc att gtc ttc ctc act   694
Leu Phe Lys Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr
100                 105                 110                 115

gtg gtg gct gtg gat agg tat ttc aaa gtg gtc cac ccc cac cat atg   742
Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His Pro His His Met
                120                 125                 130

gtg aat gcc atc tcc aac cgg act gcc gcc gcc acc gcc tgt gtc ctc   790
Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Thr Ala Cys Val Leu
            135                 140                 145

tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg atg gag agt cac   838
Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met Glu Ser His
        150                 155                 160
```

FIG. 2B

ctg tgt gtg cag ggg aca ctg tcg tcc tgt gag agc ttc atc atg gag 886
Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe Ile Met Glu
165 170 175

tca gcc aac ggg tgg cac gat gtc atg ttc cag ctg gag ttc ttc ctg 934
Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu Phe Phe Leu
180 185 190 195

ccc ctg aca atc atc ttg ttc tgc tcg gtc aac gtt gtt tgg agc ctg 982
Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val Trp Ser Leu
200 205 210

aga cgg agg cag cag ctg acc aga cag gct cgg atg agg agg gcc acc 1030
Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg Arg Ala Thr
215 220 225

cgg ttc atc atg gtg gtg gct tct gtg ttc atc acg tgt tac ctg ccc 1078
Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys Tyr Leu Pro
230 235 240

agc gtg ctg gct agg ctc tac ttc ctc tgg acg gtg ccc act agt gcc 1126
Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Thr Ser Ala
245 250 255

tgt gac ccc tct gtc cac aca gcc ctc cac gtc acc ctg agc ttc acc 1174
Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu Ser Phe Thr
260 265 270 275

tac ctg aac agt atg ctg gat ccc ctt gta tat tac ttc tca agc ccc 1222
Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro
280 285 290

tcg ctc ccc aaa ttc tac gcc aag ctc aca atc tgc agc ctg aag ccc 1270
Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser Leu Lys Pro
295 300 305

aaa cgc cca gga cgc acg aag acg cgg agg tca gaa gag atg cca att 1318
Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu Met Pro Ile
310 315 320

tcg aac ctc tgc agt aag agc tcc atc gat ggg gca aat cgt tcc cag 1366
Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn Arg Ser Gln
325 330 335

agg cca tct gac ggg cag tgg gat ctc caa gtg tgt tgaatgccat 1412
Arg Pro Ser Asp Gly Gln Trp Asp Leu Gln Val Cys
340 345 350

taagacaaac agcccaacaa cgaggcagag aaatgggcaa tgtgagttaa atctgaaggg 1472

tggaggactt gaagatgtcc cctcccactc ttagctgtat ctttctcact caggtagaaa 1532

tgggatccac cctgcttgac cttttccaga aggttccaaa ccggttggtt gtgtttaaat 1592

FIG. 2C

actctgatag caatggtgaa ggggcagcgt gtgagtgtga aggaaaccgt gggtgtcggg 1652

ttaggaacta cctggagccc gtgtcgcttt gcatggctga gaaaagcggt atgagcctgg 1712

ctgggtcttg ttctagctcg gagagagtta acgatctcaa taactcgtcg gtatttcctg 1772

gactgaaaaa aatagaaact gcactgagtc aatacactta tttccagctg agcgagaccc 1832

tttactgcag gacacccgga cctagccgtt tttttaaatc ttccctgggg agcctccaca 1892

catttcaagg tttgaacatc caggtggccc aggagggcag caaaaagaat ctattctaac 1952

cttgctggcg ccacgatatt ttgctgattt taagtggttt catcctttgt ttttcttttg 2012

tttgcatttc aaagaagatg ctgagggact tgtccacctg atatcagcta tcgtttctcc 2072

agtgggaact gagagcctgt ttacggcagc aatggtgggg ggggggtgct tcctggtatt 2132

tgggatgggt taattcaagc atggttgttc ttcactgctt aatgcatgaa tttgagctga 2192

aatcctccct tctcaagtct ttgtttaatc cacagtatgt tgtcccaccc tgtccagcat 2252

cctcgtctgt tttgtctttg gtgctgggca ttgaacttgg gaccttattc gagccaggca 2312

agcactgacc actgaactgc actcccaaac cccttgtgcc ccttttagct gtagcgttgt 2372

tagccaactt ttgggagaaa gcaaagcact agaggtggca gcaacagttt agctcaatgt 2432

cctttcgtca gtgtctagac ttctggtcag ccatccgggt ctcctattgg gggcctccct 2492

caagcacata tgttctccca aatactaccc agaattctca cagctaggtg attctgtgaa 2552

agtccaggct gcccctgtcc tggagaagga gaaatagaat ccgtgttaac cttagtccca 2612

ctttcaagcc acaaaagtgg tgacagccat tcactctctc cagttcccag ggtactctcc 2672

ccagggaagg gaccttgaca tttatgtcta aagacataaa ttagatgctc ctcaaggttg 2732

tccctgtggc ttcctttgcc agaggtgttg aagcctaggt gcgaaaatca gtctgactgc 2792

agggctggtg agaaggctca gtaggtaaac aggtctgccg ccaagccacc aacctgagta 2852

tccctgagac ccacgtggta ggagaacacc aaatcccaaa ggtggttctg tcctccacct 2912

atgttcacgc atgcgcacat gcacgcatgc gcacgcgcgc acacccaccc accaaataca 2972

ttaatgcaat aaaaatttta ttggctacac ggtcaagttt gaatcttagt ttaaatgctt 3032

attagacatg tgctcgtagg gaagacttta tttaacccca ctcagttttg atgttcagca 3092

gggttaatac tgatgccaaa gggtttggga gcaaattcaa tgactgtaca ctcataagca 3152

tgagaaatct gttgttccca ggtctgcccg gaagaagacc atgtgcgtgt agtagttgat 3212

FIG. 2D

```
aaataaatag ttgctgaaca actataatcg ctccaaaaa                    3251
```

FIG. 3A

```
tggtacgcct gcaggtaccg gtccggaatt cccgggtcga cccacgcgtc cgcaaaacta 60

gaaaagcaaa atcgtcccca ggggtggacc cagcgacaag tctgctgcgt ggctggcatc 120

agacccccaa gctgcagcct ggcaatgtac gcttttggaa aactgctctc gcctcagagc 180

ctgacccagc tgcaggcttc acctctgtag gggacatgca gcttgtgatc caggctgagg 240

agaaaggacc tgctgtcggc tttcatttcc tgactgaagt tgggtgatga ggttaggggc 300

ccagctgcca aggggaacca tagtgttcag ataggcagct gtgcctttgt gtcagccacc 360

tagg atg ctc ttc ctc tct ccg agt gct atg gac aac ggg tcg tgc tgt  409
     Met Leu Phe Leu Ser Pro Ser Ala Met Asp Asn Gly Ser Cys Cys
       1               5                  10                  15

ctc atc gag ggg gaa ccc atc acc cag gta atg cca cct tta ctc atc   457
Leu Ile Glu Gly Glu Pro Ile Thr Gln Val Met Pro Pro Leu Leu Ile
                20                  25                  30

ctg gcc ttc ctg ctt gga gcc ctg ggc aac ggc cta gcc ctg tgt ggt   505
Leu Ala Phe Leu Leu Gly Ala Leu Gly Asn Gly Leu Ala Leu Cys Gly
             35                  40                  45

ttc tgc ttt cac atg aag acc tgg aag tcg agc act att tac ctt ttc   553
Phe Cys Phe His Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe
          50                  55                  60

aac ttg gct gta gcc gat ttt ctc ctc atg atc tgc cta ccc ctt cgg   601
Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg
      65                  70                  75

aca gac tac tac ctc aga cgt agg cat tgg att ttg ggg gat att ccc   649
Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ile Leu Gly Asp Ile Pro
  80                  85                  90                  95

tgc cgc ctg gtc ctc ttc atg ctg gcc atg aat agg gcc gga agc att   697
Cys Arg Leu Val Leu Phe Met Leu Ala Met Asn Arg Ala Gly Ser Ile
                100                 105                 110

gtc ttc ctc act gtg gtg gcc gtg gac agg tat ttc aaa gtg gtc cac   745
Val Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His
             115                 120                 125

ccc cac cat atg gtg aac gcc atc tcc aat cgg act gca gct gcc atc   793
Pro His His Met Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Ile
         130                 135                 140

gtc tgt gtc ctc tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg   841
Val Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu
     145                 150                 155
```

FIG. 3B

```
atg gag agt cac ctg tgt gtg cgg ggg atg gtg tca tct tgt gag agc   889
Met Glu Ser His Leu Cys Val Arg Gly Met Val Ser Ser Cys Glu Ser
160                 165                 170                 175

ttc atc atg gag tca gcc aac ggg tgg cac gat atc atg ttc cag ctg   937
Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu
                180                 185                 190

gag ttc ttc ctg ccc ctg acc atc atc ttg ttc tgc tcc ttc aaa gtt   985
Glu Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Phe Lys Val
            195                 200                 205

gtt tgg agc ctg aga cag agg caa cag ctg acc aga cag gct cgg atg   1033
Val Trp Ser Leu Arg Gln Arg Gln Gln Leu Thr Arg Gln Ala Arg Met
        210                 215                 220

agg agg gcc acc cgg ttc atc atg gtg gtg gct tcc gtg ttc atc acg   1081
Arg Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr
    225                 230                 235

tgt tac ctg ccc agc gtg ttg gcg agg ctc tac ttc ctc tgg acg gtg   1129
Cys Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val
240                 245                 250                 255

ccc tcc agt gct tgt gac ccc tct gtc cac ata gct ctc cat gtc acc   1177
Pro Ser Ser Ala Cys Asp Pro Ser Val His Ile Ala Leu His Val Thr
                260                 265                 270

ctg agt ctc acc tac ctg aac agc atg ctg gac cct ctt gtg tac tac   1225
Leu Ser Leu Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
            275                 280                 285

ttt tca agc ccc tcg ttc ccc aaa ttc tac gcc aag ctc aaa atc cgc   1273
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Ala Lys Leu Lys Ile Arg
        290                 295                 300

agc ttg aaa ccc aga cgc cca gga cgc tcg cag gca cgg agg tcg gaa   1321
Ser Leu Lys Pro Arg Arg Pro Gly Arg Ser Gln Ala Arg Arg Ser Glu
    305                 310                 315

gag atg cca att tcg aat ctc tgt cgt aag agt tcc acc gat gtg gta   1369
Glu Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val
320                 325                 330                 335

aat agt tcc cag agg ccg tct gac ggg cag tgg ggt ctc caa gtg tgt   1417
Asn Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
                340                 345                 350

tgaatgccat gaagacaaat ggcccagcag caaagcagag acctgggcaa ctgtgagtta 1477

aatctgaagg gtgagggact tgaaaaatga cagcccccc ccccgcccca cccgcccgcc 1537

cgccccgctc tttctcagct gtgtctttct cactcaagta gaagcaaaat ctaaaaaaaa 1597
```

FIG. 3C

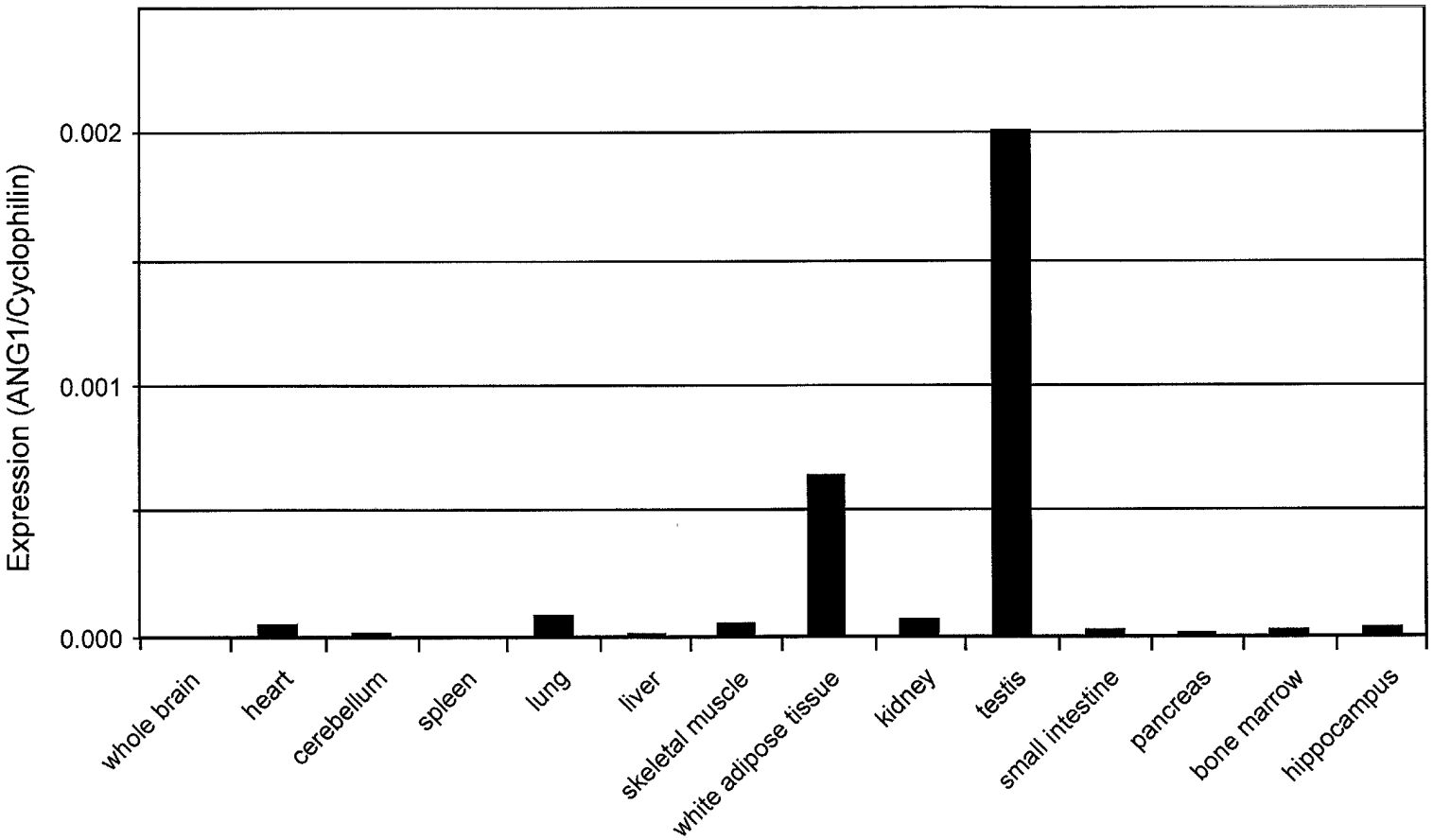
aaaaaaaaaa aaaaaaaaaa agggcggccg ctctagagga tccaagctta cgtacgcgtg 1657

catgcgacgt c 1668

FIG. 4

```
                                                TM1
hu_GPCR     1          MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCF   42
mu_GPCR     1 MPVLSPTAMDNGSCCLIEGEPISQVMPPLLILVFVLGALGNGIALCGFCF   50
ra_GPCR     1 MLFLSPSAMDNGSCCLIEGEPITQVMPPLLILAFLLGALGNGLALCGFCF   50
                  * ***** ***. *.********. *.*******.*******

                                TM2          extracellular loop 1
hu_GPCR    43 HMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGL   92
mu_GPCR    51 HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYYLRRRHWIFGDIACRLVL  100
ra_GPCR    51 HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYYLRRRHWILGDIPCRLVL  100
              ****** **.***************** ***********  *** **. *

                    TM3                                        TM4
hu_GPCR    93 FTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLWAL  142
mu_GPCR   101 FKLAMNRAGSIVFLTVVAVDRYFKVVHPHHMVNAISNRTAAATACVLWTL  150
ra_GPCR   101 FMLAMNRAGSIVFLTVVAVDRYFKVVHPHHMVNAISNRTAAAIVCVLWTL  150
              * ***************** ********** **.**.* **   * **.*

                              extracellular loop 2          TM5
hu_GPCR   143 VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGII  192
mu_GPCR   151 VILGTVYLLMESHLCVQGTLSSCESFIMESANGWHDVMFQLEFFLPLTII  200
ra_GPCR   151 VILGTVYLLMESHLCVRGMVSSCESFIMESANGWHDIMFQLEFFLPLTII  200
              *********.* ****.    ***************.*******.** **

                                                      TM6
hu_GPCR   193 LFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLY  242
mu_GPCR   201 LFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY  250
ra_GPCR   201 LFCSFKVVWSLRQRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY  250
              ****  .*****.****.*****..********* ********** ****

                extracellular
                   loop 3             TM7
hu_GPCR   243 FLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL  292
mu_GPCR   251 FLWTVPTSACDPSVHTALHVTLSFTYLNSMLDPLVYYFSSPSLPKFYAKL  300
ra_GPCR   251 FLWTVPSSACDPSVHIALHVTLSLTYLNSMLDPLVYYFSSPSFPKFYAKL  300
              ******.******** ***.*** **.*************** **** **


hu_GPCR   293 KICSLKPKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHI  342
mu_GPCR   301 TICSLKPKRPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQWDLQV  350
ra_GPCR   301 KIRSLKPRRPGRSQARRSEEMPISNLCRKSSTDVVNSSQRPSDGQWGLQV  350
               * ****..**.....* ********  .*.    *  *  *****  ..


hu_GPCR   343 VEWH 346
mu_GPCR   351 C    351
ra_GPCR   351 C    351
```

FIG. 5


Expression (ANG1/Cyclophilin)
0.002
0.001
0.000
whole brain
heart
cerebellum
spleen
lung
liver
skeletal muscle
white adipose tissue
kidney
testis
small intestine
pancreas
bone marrow
hippocampus